Amendments to the specification:

Please also amend the specification as follows:

In the Specification:

At paragraph 7:

[7.] Acute Myelogenous Leukemia (AML) is a heterogeneous group of neoplasms with a progenitor cell that, under normal conditions, gives rise to terminally differentiated cells of the myeloid series (erythrocytes, granulocytes, monocytes, and platelets). As in other forms of neoplasia, AML is associated with acquired genetic alterations that result in replacement of normally differentiated myeloid cells with relatively undifferentiated blasts, exhibiting one or more type of early myeloid differentiation. AML generally evolves in the bone marrow and, to a lesser degree, in the secondary hematopoietic organs. AML primarily affects adults, peaking in incidence between the ages of 15-40 ~~years~~, but it is also known to affect both children and older adults. Nearly all patients with AML require treatment immediately after diagnosis to achieve clinical remission, in which there is no evidence of abnormal levels of circulating undifferentiated blast cells.

At paragraph 9:

[9.] Several other humanized and chimeric antibodies are under development or are in clinical trials. In addition, a humanized Ig that specifically reacts with CD33 antigen, expressed both on normal myeloid cells as well as on most types of myeloid leukemic cells, was conjugated to the anti-cancer drug calicheamicin, CMA-676 (Sievers *et al., Blood Supplement,* 308, 504a (1997)). This conjugate, known as the drug MYLOTARG® ~~Mylotarg~~, has recently received FDA approval (Caron *et al., Cancer Supplement,* 73, 1049-1056 (1994)). In light of its cytolytic activity, an additional anti-CD33 antibody (HumM195), currently in clinical trials, was conjugated to several cytotoxic agents, including the gelonin toxin (McGraw et al., *Cancer Immunol. Immunother,* 39, 367-374 (1994)) and radioisotopes ^{131}I (Caron et al., *Blood* 83, 1760-

1768 (1994)), ^{90}Y (Jurcic et al., *Blood Supplement,* 92, 613a (1998)) and ^{213}Bi (Humm et al., *Blood Supplement,* 38:231P (1997)).

At paragraph 57:

[57.] Conservative amino acid substitution is defined as a change in the amino acid composition by way of changing one or two amino acids of a peptide, polypeptide or protein, or fragment thereof. The substitution is of amino acids with generally similar properties (e.g., acidic, basic, aromatic, size, positively or negatively charged, polar, non-polar) such that the substitutions do not substantially in a major way alter peptide, polypeptide or protein characteristics (e.g., charge, isoelectric point ~~IEF~~, affinity, avidity, confonnation, solubility) or activity. Typical substitutions that may be performed for such conservative amino acid substitution may be among the groups of amino acids as follows:

(i) glycine (G), alanine (A), valine (V), leucine (L) and isoleucine (I)
(ii) aspartic acid (D) and glutamic acid (E)
(iii) alanine (A), serine (S) and threonine (T)
(iv) histidine (H), lysine (K) and arginine (R)
(v) asparagine (N) and glutamine (Q)
(vi) phenylalanine (F), tyrosine (Y) and tryptophan (W)

At paragraph 68:

[68.] An anti-leukemia agent is an agent with anti-leukemia activity. For example, anti-leukemia agents include agents that inhibit or halt the growth of leukemic or immature pre-leukemic cells, agents that kill leukemic or pre-leukemic cells, agents that increase the susceptibility of leukemic or pre-leukemic cells to other anti-leukemia agents, and agents that inhibit metastasis of leukemic cells. In the present invention, an anti-leukemia agent may also be agent with anti-angiogenic activity that prevents, inhibits, retards or halts vascularization of tumors.

At paragraph 73:

[73.] The term "epitope" is used herein to mean the antigenic determinant or antigen site that interacts with an antibody, antibody fragment, antibody complex or a complex comprising a binding fragment thereof or T-cell receptor. The term epitope is used interchangeably herein with the ~~tersm~~ terms ligand, domain, and binding region.

At paragraph 74:

[74.] A given cell may express on its surface a protein having a binding site (or epitope) for a given antibody, but that binding site may [[be]] exist in a cryptic form (e.g., be sterically hindered or be blocked, or lack features needed for binding by the antibody) in the cell in a state, which may be called a first stage (stage I). Stage I may be, for example, a normal, healthy, non-diseased status. When the epitope exists in cryptic form, it is not recognized by the given antibody, i.e., there is no binding of the antibody to this epitope or to the given cell at stage I. However, the epitope may be exposed by, e.g., undergoing modifications itself, or being unblocked because nearby or associated molecules are modified or because a region undergoes a conformational change. Examples of modifications include changes in folding, changes in post-translational modifications, changes in phospholipidation, changes in sulfation, changes in glycosylation, and the like. Such modifications may occur when the cell enters a different state, which may be called a second stage (stage II). Examples of second states, or stages, include activation, proliferation, transformation, or in a malignant status. Upon being modified, the epitope may then be exposed, and the antibody may bind.

At paragraph 88:

[88.] Phagemids are plasmid vectors designed to contain an origin of replication from a filamentous phage, such as M13 ~~m13~~ or ~~of~~ fd.

At paragraph 109:

[109.] In one embodiment of the invention, a tag is inserted or attached to the Fv peptide or polypeptide to aid in the preparation and identification thereof, and in

diagnostics. The tag can later be removed from the molecule. The tag may be, but is not limited to, the following tags: AU1, AU5, BTag, c-myc, FLAG, Glu-Glu, HA, His6 (SEQ ID NO: 204), HSV, HTTPHH (SEQ ID NO: 205), IRS, KT3, Protein C, S-TAG® ~~S•Tag®~~, T7, V5, VSV-G (Jarvik and Telmer, *Ann. Rev. Gen.*, 32, 601-618 (1998)), and KAK (lysine-alanine-lysine) (SEQ ID NO: 238). The tag is preferably c-myc or KAK (SEQ ID NO: 238).

At paragraph 110:

[110.] The two variable chains of the Fv molecule of the present invention may be connected or linked together by a spacer of 0-20 amino acid residues in length. The spacer may be branched or unbranched. Preferably, the linker is 0-15 amino acid residues, and most preferably the linker is $(Gly_4Ser)_3$ (SEQ ID NO: 206) to yield a single chain Fv ("scFv"). The scFv is obtainable from a phage display library.

At paragraph 128:

[128.] The spacer region of the scFv may be linear or branched, and is generally comprised of glycine and serine residues, in multiples of the formula $(Gly_4Ser)_n$, (SEQ ID NO: 233) and is generally between a total of 0-20 amino acids in length, preferably 0-15 amino acids long and linear. By changing the spacer length as appropriate, a variety of multimers can be obtained. In an embodiment of the invention, the spacer is 0-5 amino acids in length. In another embodiment, the spacer is < 3 amino acids long (as detailed below).

At paragraph 129:

[129.] An example of an amino acid sequence of a scFv molecule of the subject invention follows (SEQ ID NOS: 207 & 25, respectively):

```
        ATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCCAGCCGGCC
1        M  K  Y  L  L  P  T  A  A  A  G  L  L  L  L  A  A  Q  P  A
         ------------------------------------------------------------

61      ATGGCCGAGGTGCAGCTGGTGGAGTCTGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTG
```

```
21    M  A  E  V  Q  L  V  E  S  G  G  G  V  V  R  P  G  G  S  L
      ------

121   AGACTCTCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGGCATGAGCTGGGTCCGC

41    R  L  S  C  A  A  S  G  F  T  F  D  D  Y  G  M  S  W  V  R

181   CAAGCTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTATTAATTGGAATGGTGGTAGCACA

61    Q  A  P  G  K  G  L  E  W  V  S  G  I  N  W  N  G  G  S  T

241   GGTTATGCAGACTCTGTGAGGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCC

81    G  Y  A  D  S  V  K  G  R  F  T  I  S  R  D  N  A  K  N  S

301   CTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACCGGCCGGTGTATTACGTGGCAAGA

101   L  Y  L  Q  M  N  S  L  R  A  E  D  T  A  V  Y  Y  C  A  R

361   ATGAGGGCTCCTGTGATTTGGGCCCAAGTAACCCTGGTCACCGTGTCGAGAGTGGGAGGC

121   M  R  A  P  V  I  W  G  Q  G  T  L  V  T  V  S  R  G  G  G

421   GGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGTCTGAGCTGACACAGGACCCTGCT

141   G  S  G  G  G  G  S  G  G  G  G  S  S  E  L  T  Q  D  P  A

481   GTGTCTGTGGCCTTGGGACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGC

161   V  S  V  A  L  G  Q  T  V  R  I  T  C  Q  G  D  S  L  R  S

541   TATTATGCAAGCTGGTACCAGCAGAAGCAGGACCAGGCCCCTTGTCTTGTCATCATGGGT

181   Y  Y  A  S  W  Y  Q  Q  K  P  G  Q  A  P  V  L  V  I  Y  G

601   AAAAACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCAGCTCAGGAAACACA

201   K  N  N  R  P  S  G  I  P  D  R  F  S  G  S  S  S  G  N  T

661   GCTTCCTTGACCATCACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAACTCC

221   A  S  L  T  I  T  G  A  Q  A  E  D  E  A  D  Y  Y  C  N  S

721   CGGGACAGCAGTGGTAACCATGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT

241   R  D  S  S  G  N  H  V  V  F  G  G  G  T  K  L  T  V  L  G

781   GCGGCCGCAGAACAAAAACTCATCTCAGAAGAGGATCTGAATGGGGCCGCATAG

261   A  A  A  E  Q  K  L  I  S  E  E  D  L  N  G  A  A
                  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

At paragraph 130:

[130] The leader sequence is underlined with a dashed line (amino acids 1-22). The V_H region is encoded by the bolded amino acid sequence (amino acids 23-120 (SEQ ID NO: 61). This specific clone is derived from the germline V_H3-DP32; however, the germline of each clone is dependent on its particular origin (see below). The amino acid sequence enclosed in a box (amino acids 121-126) encodes [[for]] the V_H-CDR3 sequence, the hypervariable region among all clones derived from this library. The spacer region joining the V_H and the V_L regions is a flexible polypeptide, encoded by amino acids shown by italics. Finally the V_L region is presented (amino acids 154-260, SEQ ID NO: 234). The fused V_L fragment in all the clones is derived from a single unmutated V gene of germline IGLV3SI, and is here followed by the c-myc tag, underlined with a wavy line (amind acids 264-277, SEQ ID NO: 236). The full amino acid sequence is identical to SEQ ID NO:25. The Y1-scFv lacking an N-terminal leader, the C-terminal linker and the C-terminal myc tag is at amino acids 21-260 and is SEQ ID NO: 235.

At paragraph 182:

[182.] In this system, the phage library (as described herein above) was designed to display scFvs, which can fold into the monovalent form of the Fv region of an antibody. Further, and also discussed herein above, the construct is suitable for bacterial expression. The genetically engineered scFvs comprise heavy chain and light chain variable regions joined by a contiguously encoded 15 amino acid flexible peptide spacer. The preferred spacer is $(Gly_4Ser)_3$ (SEQ ID NO: 206). The length of this spacer, along with its amino acid constituents provides for a nonbulky spacer, which allows the V_H and the V_L regions to fold into a functional Fv domain that provides effective binding to its target.

At paragraph 185:

[185.] To compare the binding of the Y1 scFv monomer (also referred to as CONY1) with the YI dimer, binding competition experiments were done in vitro on KG-

1 cells. In addition, these experiments also compared the binding of the full YI IgG to the scFv Y1 monomers. To perform this study, Y1 IgG was labeled with biotin. This study revealed that Y1 IgG competed with IgG Y1-Biotin. Non-relevant human IgG did not compete with the labeled Y1 IGg. Y1 scFvs (5 μg and 10 μg) partially competed with Y1 IgG-Biotin (50 ng). The studies also showed that 1 ng of IgGY1-FITC bound to KG-1 cells (without serum) to the same extent as 1 μg of scFv-FITC, but in the presence of serum, most of Y1 IgG binding was "blocked." These studies also showed that the binding of the Y1 dimer is at least 20-fold higher than that of the scFV monomer as analyzed by radioreceptor assay, ELISA or FACS.

At paragraph 186:

[186.] In yet another emobodiment, a lysine-alanine-lysine was added in addition to the cysteine at the carboxyl end (referred to as YI-cys-KAK[[kak]] scFv). The amino acid sequence of this scFv construct is reproduced below (SEQ ID NO: 208).

```
1   MEVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTG  60
61  YADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARMRAPVIWGQGTLVTVSRGGGG 120
121 SGGGGSGGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGK 180
181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGG 240
241 GGCKAK
```

At paragraph 187:

[187.] The Y1-cys-KAK [[Y1-cys-kak]] was produced in a λ-pL vector in bacteria. Expression in the λ-pL vector was induced by increasing the temperature to 42EC. Inclusion bodies were obtained from induced cultures and semi-purified by aqueous solutions, to remove unwanted soluble proteins. The inclusion bodies were solubilized in guanidine, reduced by DTT ~~DTE~~, and refolded *in vitro* in a solution based on arginine/oxidized-[ox-]glutathione. After refolding, the protein was dialyzed and concentrated by tangential flow filtration to a buffer containing urea [Urea]/phosphate

buffer. The protein was repurified and concentrated by ionic-chromatography in an SP-column.

At paragraph 194:

[194.] Varying the length of the spacers is yet another preferred method of forming dimers, trimers, and tetramers (often referred to in the art as diabodies, triabodies and tetrabodies, respectively). Dimers are formed under conditions where the spacer joining the two variable chains of a scFv is shortened ~~to generally~~. This shortened spacer prevents the two variable chains from the same molecule from folding into a functional Fv domain. Instead, the domains are forced to pair with complimentary domains of another molecule to create two binding domains. In a preferred method, a spacer of only 5 amino acids (Gly_4Ser) was used for diabody construction. This dimer can be formed from two identical scFvs, or from two different populations of scFvs and retain the selective and/or specific enhanced binding activity of the parent scFv(s), and/ or show increased binding strength or affinity.

At paragraph 224:

[224.] In yet another embodiment, the link between the peptide and the pharmaceutical agent is affected by a linker compound. As used herein in the specification and in the claims, a linker compound is defined as a compound that joins two or more moieties together. The linker can be straight-chained or branched. The branched linker compound can be composed of a double-branch, triple branch, or quadruple or more branched compound. The linker compound may be, but is not limited to, a dicarboxylic acid, a malemido hydrazide, PDPH, a carboxylic acid hydrazide, and a small peptide. Examples of other linker compounds include: Dicarboxylic acids such as succinic acid, glutaric acid, and adipic acid; Maleimido hydrazides such as N-[ε-maleimidocaproic acid] hydrazide, 4-[N-maleimidomethyl]cyclohexan-1-carboxylhydrazide, and N-[κ-maleimidoundecanoic acid] hydrazide] ~~N-[κ-maleimidoundecanoic acid hydrazide]~~; PDPH linker such as (3-[2-pyridyldithio]propionyl hydrazide) conjugated to sulfurhydryl reactive protein; Carboxylic acid hydrazides

selected from 2-5 carbon atoms; and direct coupling using small peptide linkers between the free sugar of, for example, the anti-cancer drug doxorubicin and a scFv. Small peptides include, but are not limited to AU1, AU5, BTag, c-myc, FLAG, Glu-Glu, HA, His6 (SEQ ID NO: 204), HSV, HTTPHH (SEQ ID NO:205), IRS, KT3, Protein C, S-TAG® ~~S•Tag®~~, T7, V5, VSV-G, and KAK Tag (SEQ ID NO:238).

At paragraph 275:

[275.] **2.3 Sequence analysis:** The encoded scFv DNA of ~800bp within the phagemid particles was amplified by PCR using an upstream primer #203743 (5'-GAAATACCTATTGCCTACGG) (SEQ ID NO: 209) and a downstream primer #181390 (5'-TGAATTTTCTGTATGAGG) (SEQ ID NO: 210). DNA fragments were fully sequenced from both ends by the automatic ABI PRISM DNA sequencer (310 Genetic Analyzer, Perkin Elmer) using ABI PRISM Big Dye termination cycle sequencing kit and the above primers. Two additional primers, primer #191181 (5%-CGATCCGCCACCGCCAGAG) (SEQ ID NO: 211) and its complementary primer # 191344 (5'-CTCTGGCGGTGGCGGATCG) (SEQ ID NO: 212), which are located at the flexible polypeptide junction region between the heavy and light chains, were used for sequencing.

At paragraph 328:

[328.] The amino acid sequences displayed in the V_H-CDR3 and their frequency in the tested clone output are summarized in Table 2 (SEQ ID NOS: 9-18, respectively, in order of appearance).

At paragraph 338:

[338.] **6.2.2 Clone Sequence Results for YPR and YPNR Protocols:**

Several clones from the third panning from both protocols were selected for sequencing. The amino acid sequences presented in Table 5 are those of the CDR3 regions of the heavy chain (V_H-CDR3). The germline and the frequency with which the sequences

appeared in the R3 output are also indicated in this table (SEQ ID NOS: 8 and 19-24, respectively, in order of appearance).

At paragraph 363:

[363.] **8.7 Y1 is a specific clone to leukemia cells:** The Y1 cassette belongs to the V_H-DP32 germline. Several other clones, originating from the same germline, were isolated and are detailed in Example 6. These clones include Y17, Y-27, and Y-44. The primary sequences (i.e., germline cassette) of all these clones differ in their CDR3 regions only. However, only Y1 shows selectivity to leukemic cells. The CD3 sequences of these clones are summarized in Table 10, and the binding profiles of the clones are summarized in Table 11 (SEQ ID NOS: 8 and 20-22, respectively, in order of appearance).

At paragraph 365:

[365.] **9.1 Construction of triabodies**: The vector pHEN-Y1, encoding the original Y1, was amplified using PCR for both the V_L and the V_H regions, individually. The sense oligonucleotide 5'-AACTCGAGTGAGCTGACACAGGACCCT (SEQ ID NO: 213), and the anti-sense oligonucleotide 5'-TTTGTCGACTCATTTCTTTTTTGCGGCCGCACC (SEQ ID NO: 214) were used for the V_L PCR reaction. The cDNA product of the expected size of ~350 bp was purified, sequenced, and digested with XhoI and NotI restriction enzymes.

At paragraph 366:

[366.] The same procedure was employed to amplify the V_H region (using the sense oligonucleotide 5'-ATGAAATACCTATTGCCTACGG (SEQ ID NO: 215) and anti-sense oligonucleotide 5'-AACTCGAGACGGTGACCAGGGTACC) (SEQ ID NO: 216). The V_H PCR product was digested with NcoI and XhoI restriction enzymes. A triple ligation procedure into the pHEN vector, pre-digested with NcoI-NotI, was employed. The final vector was designated pTria-Y1.

At paragraph 369:

[369.] The pTria-Y1 vector from above was linearized with XhoI restriction enzyme, and synthetic complimentary double stranded oligonucleotides (5'-TCGAGAGGTGGAGGCGGT (SEQ ID NO: 217) and 5' TCGAACCGCCTCCACCTC) (SEQ ID NO: 218) were pre-annealed and ligated into the XhoI site, between the Y1-heavy and Y1-light chains. This new vector was designated pDia-Y1. As described for the triabodies, the DNA sequence and protein expression was confirmed.

At paragraph 375:

[375.] **Production of Y1-cys-KAK ~~kak~~ (cysteine dimer)**

At paragraph [376]:

[376.] One liter of λpL-y1-cys-KAK ~~kak~~ bacterial culture was induced at 42°C for 2-3 hrs. This culture was centrifuged at 5000 RPM for 30 minutes. The pellet was resuspended in 180 ml of TE (50mM Tris-HCl pH 7.4, 20mM EDTA). 8 ml of lysozyme (from a 5 mg/ml stock) was added and incubated for 1 hr. 20 ml of 5M NaCl and 25 ml of 25% Triton was added and incubated for another hour. This mixture was centrifuged at 13000 RPM for 60 minutes at 4° C. The supernatant was discarded. The pellet was resuspended in TE with the aid of a tissuemiser (or homogenizer). This process was repeated 3-4 times until the inclusion bodies (pellet) were gray/light brown in color. The inclusion bodies were solubilized in 6M Guanidine-HCl, 0.1M Tris pH 7.4, 2 mM EDTA (1.5 grams of inclusion bodies in 10 ml solubilization buffer provided ~10 mg/ml soluble protein). This was incubated for at least 4 hrs. The protein concentration was measured and brought to a concentration of 10 mg/ml. DTT ~~DTE~~ was added to a final concentration of 65 mM and incubated overnight at room temperature. Re-folding was initiated by dilution of 10 ml of protein (drop by drop) to a solution containing 0.5 M Arginine, 0.1 M Tris pH 8, 2 mM EDTA, 0.9 mM GSSG. The re-folding solution was incubated at ~10° C for 48 hrs. The re-folding solution containing the protein was dialyzed in a buffer containing 25 mM Phosphate buffer pH 6, 100 mM Urea, and

concentrated to 500 ml. The concentrated/dialyzed solution was bound to an SP-sepharose column, and the protein was eluted by a gradient of NaCl (up to 1M).

At paragraph [387]:

[387.] A construct was designed where the following sequence, LNDIFEAQKIEWHE (SEQ ID NO: 219), was added at the C-terminus of the Y1 by PCR and cloning into an IPTG inducible expression vector cassette. The clone was named Y1-biotag. This sequence is a substrate for the enzyme BirA, that in the presence of free biotin, the enzyme is capable of covalently connecting biotin to the lysine (K) residue (Phenotypic analysis of antigen-specific T lymphocytes. Science. 1996 Oct 4;274(5284):94-6, Altman JD et al). This construct was produced as inclusion bodies in BL21 bacterial cells. Refolding was performed as described previously. Inclusion bodies were solubilized in guanidine-DTT ~~guanidine-DTE~~. Refolding was done by dilution in a buffer containing arginine-Tris-[[tris-]]EDTA. Dialysis and concentration was performed followed by HiTrapQ ionic exchange purification.

At paragraph 390:

[390.] The sequence of Yl-biotag is as follows (SEQ ID NO: 220):

1 MEVQLVESGG GVVRPGGSLR LSCAASGFTF DDYGMSWVRQ
41 APGKGLEWVS GINWNGGSTG YADSVKGRFT ISRDNAKNSL
81 YLQMNSLRAE DTAVYYCARM RAPVIWGQGT LVTVSRGGGG
121 SGGGGSGGGG SSELTQDPAV SVALGQTVRI TCQGDSLRSY
161 YASWYQQKPG QAPVLVIYGK NNRPSGIPDR FSGSSSGNTA
201 SLTITGAQAE DEADYYCNSR DSSGNNVVFG GGTKLTVLGG
241 GGLNDIFEAQ KIEWHE

At paragraph 393:

[393.] **10.1 A leader sequence compatible for a mammalian expression system:** An exchangeable system was designed to allow convenient insertion of

~~elerAents~~ elements required for a full IgG molecule. The following complimentary double stranded oligonucleotides encoding a putative leader sequence were synthesized, annealed, and ligated into the XhoI site of mammalian expression vector (under the SRα5 promoter). 5'-
TCGACCTCATCACCATGGCCTGGGCTCTGCTGCTCCTCACCCTCCTCACTCAG
GACACAGGGTCCTGGGCCGAT (SEQ ID NO: 221) and 5'-
GATCGATTGCACCAGCTGGATATCGGCCCAGGACCCTGTGTCCTGAGTGAGG
AGGGTGAGGAGCAGCAGCCCAGGCCATGGTGATGAGG (SEQ ID NO: 222).
Upstream of the initiation ATG codon, two Kozak elements were included. In addition, an internal EcoRV site was introduced between the putative cleavage site of the leader sequence and the XhoI site to allow subcloning of the variable regions. This modified vector was designated pBJ-3. At paragraph 395:

At paragraph 395:

[395.] **10.3 The oligonucleotides**
5'-TTTGATATCCAGCTGGTGGAGTCTGGGGGA (sense) (SEQ ID NO: 223) and 5'-
GCTGACCTAGGACGGTCAGCTTGGT (anti-sense) (SEQ ID NO: 224) were used for the V_L PCR reaction. The cDNA product of the expected size of ~350 bp was purified, sequenced and digested with EcoRV and AvrII restriction enzymes. The same procedure was employed to amplify and purify the V_H cDNA region, using the sense and the anti-sense oligonucleoitides
5'-GGGATATCCAGCTG(C/G)(A/T)GGAGTCGGGC (SEQ ID NO: 225) and 5'-
GGACTCGAGACGGTGACCAGGGTACCTTG, respectively (SEQ ID NO: 226).

At paragraph 397:

[397.] 10.4.1 For the constant CL-λ3 region, RT-PCR was performed on mRNA extracted from a pool of normal peripheral B-cells (CD 19+cells) in combination with the sense 5'-CCGTCCTAGGTCAGCCCAAGGCTGC (SEQ ID NO: 227) and the anti-sense 5'- TTTGCGGCCGCTCATGAACATTCTGTAGGGGCCACTGT (SEQ ID NO: 228) oligonucleotides. The PCR product of the expected size (~400 bp) was purified,

sequenced, and digested with AvrII and NotI restriction enzymes.

At paragraph 398:

[398.] **10.4.2 For the constant IgGI regions** (γ chain), a human B cell clone (CMV - clone #40), immortalized at BTG, was selected for PCR amplification. This clone was shown to secrete IgG1 against human CMV and was also shown to induce ADCC response in *in-vitro* assays. For the CH1-CH3 cDNA, oligonucleotides 5'-CCGCTCGAGTGC(T/C)TCCACCAAGGGCCCATC(G/C)GTCTTC (sense) (SEQ ID NO: 229) and 5'-TTTGCGGCCGCTCATTTACCC(A/G)GAGACAGGGAGAGGCT (anti-sense) (SEQ ID NO: 230) were synthesized and used for PCR amplification. As described for the CL cDNA encoding sequence, the PCR product of expected size (~1500 bp) was purified, sequenced, and digested with AvrII and NotI restriction enzymes.

At paragraph 402:

[402.] **10.7.1 The ORF of Y1-IgG-HC (V_H, C_H1 C_H2 C_H3)** (SEQ ID NO 231 and 26, respectively)

```
1      ATGGCCTGGGCTCTGCTGCTCCTCCACCCTCCTCACTCAGGACACAGGGTCCTGGGCCGAT
1       M  A  W  A  L  L  L  L  T  L  L  T  Q  D  T  G  S  W  A  D

61     ATCCAGCTGGTGGAGTCTGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCC
21      I  Q  L  V  E  S  G  G  G  V  V  R  P  G  G  S  L  R  L  S

121    TGTGCAGCCTCTGGATTCACCTTTGATGATTATGGCATGAGCTGGGTCCGCCAAGCTCCA
41      C  A  A  S  G  F  T  F  D  D  Y  G  M  S  W  V  R  Q  A  P

181    GGGAAGGGGCTGGAGTGGGTCTCTGGTATTAATTGGAATGGTGGTAGCACAGGTTATGCA
61      G  K  G  L  E  W  V  S  G  I  N  W  N  G  G  S  T  G  Y  A

241    GACTCTGTGAAGGGCCGATTCACCATCTCTAGAGACAACGCCAAGAACTCCCTGTATCTG
81      D  S  V  K  G  R  F  T  I  S  R  D  N  A  K  N  S  L  Y  L

301    CAAATGAACAGTCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCAAGAATGAGGGCT
101     Q  M  N  S  L  R  A  E  D  T  A  V  Y  Y  C  A  R  M  R  A

361    CCTGTGATTTGGGGCCAAGGTACCCTGGTCACCGTCTCGAGTGCTTCCACCAAGGGCCCA
121     P  V  I  W  G  Q  G  T  L  V  T  V  S  S  A  S  T  K  G  P

421    TCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGC
141     S  V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G
```

```
481   TGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTG
161    C  L  V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S  G  A  L

541   ACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
181    T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G  L  Y  S  L  S

601   AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
201    S  V  V  T  V  P  S  S  S  L  G  T  Q  T  Y  I  C  N  V  N

661   CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACT
221    H  K  P  S  N  T  K  V  D  K  R  V  E  P  K  S  C  D  K  T

721   CACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGGACTGTCAGTCTTCNTCTTC
241    H  T  C  P  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F

781   CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTG
261    P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V

841   GTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG
281    V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E

901   GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
301    V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V

961   AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC
321    S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V

1021  TCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
341    S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P

1081  ~~O~~CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC
361    R  E  P  Q  V  Y  T  L  P  P  S  R  E  E  M  T  K  N  Q  V

1141  AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGC
381    S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S

1201  AATGGGCAGCCGGAGAACAACTACAAGACCACGTCTCCCGTGCTGGACTCCGACGGCTCC
401    N  G  Q  P  E  N  N  Y  K  T  T  S  P  V  L  D  S  D  G  S

1261  TTCTTCCTCTATAGCAAGCTCACCGTGCACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
421    F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F

1321  TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
441    S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L

1381  TCTCTGGGTAAATGA
461    S  L  G  K  *
```

At paragraph 403:

[403] **10.7.2 The ORF of Y1-IgG-LC** (SEQ ID NOS: 232 and 27 respectively)

```
1    ATGGCCTGGGCTCTGCTGCTCCTCACCCTCCTCACTCAGGACACAGGGTCCTGGGCCGAT
1     M  A  W  A  L  L  L  L  T  L  L  T  Q  D  T  G  S  W  A  D

61   GCAGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGGACAGACAGTCAGGATCACA
21    A  E  L  T  Q  D  P  A  V  S  V  A  L  G  Q  T  V  R  I  T

121  TGCCAAGGACACAGCCTCAGAAGCTATTATGCAAGCTGGTACCAGCAGAAGCCAGGACAG
41    C  Q  G  D  S  L  R  S  Y  Y  A  S  W  Y  Q  Q  K  P  G  Q

181  GCCCCTGTACTTGTCATCTATGGTAAAAACAACCGGCCCTCAGGGATCCCAGACCGATTC
161   A  P  V  L  V  I  Y  G  K  N  N  R  P  S  G  I  P  D  R  F

241  TCTGGCTCCAGCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGCTCAGGCGGAAGAT
81    S  G  S  S  S  G  N  T  A  S  L  T  I  T  G  A  Q  A  E  D

301  GAGGCTGACTATTACTGTAACTCCCGGGACAGCAGTGGTAACCATGTGGTATTCGGCGGA
101   E  A  D  Y  Y  C  N  S  R  D  S  S  G  N  H  V  V  F  G  G

361  GGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG
121   G  T  K  L  T  V  L  G  Q  P  K  A  A  P  S  V  T  L  F  P

421   CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC
141    P  S  S  E  E  L  Q  A  N  K  A  T  L  V  C  L  I  S  D  F

481   TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG
161    Y  P  G  A  V  T  V  A  W  K  A  D  S  S  P  V  K  A  G  V

541   GAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGC
181    E  T  T  T  P  S  K  Q  S  N  N  K  Y  A  A  S  S  Y  L  S

601    CTGACGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCTGCCAGGTCACGCATGAAGGG
201     L  T  P  E  Q  W  K  S  H  K  S  Y  S  C  Q  V  T  H  E  G

661    AGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
221     S  T  V  E  K  T  V  A  P  T  E  C  S  *
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Please replace the Abstract on page 139 with the following new Abstract, which is submitted on a separate sheet as required by 37 C.F.R. §1.72.

The present invention is directed to novel peptides and polypeptides that specifically bind to target cells and may have anti-cancer activity, especially blood-related cancers. The present invention includes a peptide or polypeptide comprising an Fv molecule, having a heavy variable chain comprising CDR3, CDR2 and CDR1 regions comprising the amino acid sequences SEQ ID NOS:8, 115 and 114, respectively.